

STIC-Biotech/ChemLib

162174

From: Bowman, Amy
Sent: Wednesday, September 28, 2005 3:01 PM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/738,413

Hello,
I need SEQ ID NO: 1 searched in application 10/738,413, with lower and upper limits of 21 and 30 nucleobases, respectively.
Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

CNFE

Barb O Byler

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:06:54 ; Search time 1712 Seconds
(without alignments)
594.369 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usgaccugccagucgucut 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 646394

Minimum DB seq length: 21

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_dr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	13.6	64.8	26	6	AR091206 Sequence
3	13.6	64.8	26	6	AR198188 Sequence
4	13.6	64.8	26	6	AR198241 Sequence
5	13.6	64.8	26	6	AR260342 Sequence
6	13.6	64.8	26	6	AR260395 Sequence
7	13.4	63.8	25	6	AR526958 Sequence
8	13.4	63.8	25	6	128239 Sequence
9	13.4	63.8	25	6	AR195002 Sequence
10	13.4	63.8	29	6	AX183809 Sequence
11	13.2	62.9	22	6	E26686 Improved me
12	13.2	62.9	24	6	AX292533 Sequence
13	12.8	61.0	21	6	BD171375 Method fo
14	12.8	61.0	21	6	BD173609 Method of
15	12.8	61.0	22	6	AX354409 Sequence
16	12.8	61.0	22	6	CQ866237 Sequence
17	12.6	60.0	22	6	AX503893 Sequence
18	12.6	60.0	23	6	AX148231 Sequence
19	12.6	60.0	23	6	AX473373 Sequence

C 20	12.6	60.0	30	6	AR091140 Sequence
C 21	12.6	60.0	30	6	AR198175 Sequence
C 22	12.6	60.0	30	6	AR260329 Sequence
C 23	12.4	59.0	22	6	AR093096 Sequence
C 24	12.4	59.0	22	6	BD009920 BH3 inter
C 25	12.4	59.0	23	6	E10819 FITC label
C 26	12.4	59.0	28	6	AX614457 Sequence
C 27	12.2	58.1	22	6	AR093407 Sequence
C 28	12.2	58.1	22	6	AR179499 Sequence
C 29	12.2	58.1	22	6	E30932 Amplificati
C 30	12.2	58.1	23	6	AR225080 Sequence
C 31	12.2	58.1	24	6	AX290310 Sequence
C 32	12.2	58.1	25	6	E52191 Novel gene
C 33	12.2	58.1	29	6	BD170056 Novel N-a
C 34	12.2	58.1	30	10	S86546 TCR V beta
C 35	12.2	57.1	21	6	AR123316 Sequence
C 36	12.2	57.1	21	6	AR487412 Sequence
C 37	12.2	57.1	21	6	AR529674 Sequence
C 38	12.2	57.1	21	6	AX095699 Sequence
C 39	12.2	57.1	23	6	AX105351 Sequence
C 40	12.2	57.1	24	6	CQ792973 Sequence
C 41	12.2	57.1	25	6	AR117096 Sequence
C 42	12.2	57.1	25	6	AR175442 Sequence
C 43	12.2	57.1	25	6	AR238776 Sequence
C 44	12.2	57.1	25	6	AR338139 Sequence
C 45	12.2	57.1	25	6	AX609748 Sequence

ALIGNMENTS

RESULT 1	AR091153	Sequence 1273 from patent US 5994076.	26 bp	DNA	1linear	PAT 07-SEP-2000
LOCUS	AR091153					
DEFINITION	AR091153					
ACCESSION	AR091153					
VERSION	AR091153.1	GI:10017908				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 26)					
AUTHORS	Chenichik,A., Jokhadze,G. and Bibilashvili,R.					
TITLE	Methods of assaying differential expression					
JOURNAL	Patent: US 5994076-A 1273 30-NOV-1999;					
FEATURES	Location/Qualifiers					
Source	1..26					
ORIGIN	/organism="unknown"					
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Matches	11; Conservative	5; Mismatches	4; Indels	0; Gaps	0;	
Cy	1	UAGACCGCCAGUCGUCUT	20			
Db	20	TTGGCCTTGCCGTCCTCTT	1			
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LOCUS	AR091206					
DEFINITION	AR091206					
ACCESSION	AR091206					
VERSION	AR091206.1	GI:10017961				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 26)					
AUTHORS	Chenichik,A., Jokhadze,G. and Bibilashvili,R.					
TITLE	Methods of assaying differential expression					

JOURNAL Patent: US 5994076-A 1326 30-NOV-1999;
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/mol_type="unassigned DNA"

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Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGGCGUCCTT 21
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Db 4 AGGACCTTCAGTCTACTT 23

RESULT 3
AR198188/c AR198188 26 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 1273 from patent US 6352829.
DEFINITION AR198188
ACCESSION AR198188
VERSION AR198188.1 GI:20248037
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1273 05-MAR-2002;
FEATURES
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 64.8%; Score 13.6; DB 6; Length 26;
Best Local Similarity 55.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UNGACCGCCAGGCGUCCTT 20
:||||:||||:|:|
Db 20 TTGGCCTTGCCGCTGCTCTT 1

RESULT 4
AR198241 AR198241 26 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 1326 from patent US 6352829.
DEFINITION AR198241
ACCESSION AR198241
VERSION AR198241.1 GI:20248090
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1326 05-MAR-2002;
FEATURES
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 64.8%; Score 13.6; DB 6; Length 26;
Best Local Similarity 65.0%; Pred. No. 1.5e+04;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGGCGUCCTT 21
|||||:||||:|:|
Db 4 AGGACCTTCAGTCTACTT 23

RESULT 5
AR260342/c AR260342 26 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 1273 from patent US 6489455.
DEFINITION AR260342
ACCESSION AR260342
VERSION AR260342.1 GI:27310853
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 1273 03-DEC-2002;
FEATURES
source
1. .26
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 64.8%; Score 13.6; DB 6; Length 26;
Best Local Similarity 55.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UNGACCGCCAGGCGUCCTT 20
:||||:||||:|:|
Db 20 TTGGCCTTGCCGCTGCTCTT 1

RESULT 6
AR260395 AR260395 26 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 1326 from patent US 6489455.
DEFINITION AR260395
ACCESSION AR260395
VERSION AR260395.1 GI:27310906
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 1326 03-DEC-2002;
FEATURES
source
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/mol_type="genomic DNA"

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Best Local Similarity 65.0%; Pred. No. 1.5e+04;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGGCGUCCTT 21
|||||:||||:|:|
Db 4 AGGACCTTCAGTCTACTT 23

RESULT 7
AR526958/c AR526958 23 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 12 from patent US 6723534.
DEFINITION AR526958
ACCESSION AR526958
VERSION AR526958.1 GI:53913871
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Lin,H.
TITLE Purified and isolated PIWI family genes and gene products and
therapeutic and screening methods using same

JOURNAL Patent: US 6723534-A 12 20-APR-2004;
FEATURES Location/Qualifiers
SOURCE 1..23
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 80.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGACCTGCGCAGTGC 16
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16 AGGACCTGCGCAGTGC 2

RESULT 8
LOCUS 128239 25 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 15 from patent US 5569753.
ACCESSION 128239
VERSION 128239.1 GI:1819015
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Wigler,M. and Lisitsyn,N.
TITLE Cancer detection probes
JOURNAL Patent: US 5569753-A 15 29-OCT-1996;
FEATURES Location/Qualifiers
SOURCE 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 73.3%; Pred. No. 1.9e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 UAGACCTGCGCAGUG 15
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3 TAGGAAGTGCAGTGTG 17

DB 3 TAGGAAGTGCAGTGTG 17

RESULT 9
LOCUS AR195002 25 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 6350576.
ACCESSION AR195002
VERSION AR195002.1 GI:20244439
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
AUTHORS Wigler,M. and Lisitsyn,N.
TITLE Cancer detection probes
JOURNAL Patent: US 6350576-A 24 26-FEB-2002;
FEATURES Location/Qualifiers
SOURCE 1..25
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 63.8%; Score 13.4; DB 6; Length 25;
Best Local Similarity 73.3%; Pred. No. 1.9e+04;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 UAGACCTGCGCAGUG 15
|||||:|||||:
3 TAGGAAGTGCAGTGTG 17

RESULT 10
LOCUS AX183809 29 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1562 from Patent WO0142511.
ACCESSION AX183809
VERSION AX183809.1 GI:15135137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Dally,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1562 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipse
Biotechnology Corporation (CA)
FEATURES Location/Qualifiers
SOURCE 1..29
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ORIGIN

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Best Local Similarity 68.8%; Pred. No. 2e+04;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGGACCTGCGCAGUGCU 17
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10 AGGACCTGCGCAGTGT 25

DB 10 AGGACCTGCGCAGTGT 25

RESULT 11
LOCUS E26686 22 bp DNA linear PAT 18-JUN-2001
DEFINITION Improved method for measuring cytokine gene expression.
ACCESSION E26686
VERSION E26686.1 GI:13026273
KEYWORDS JP 1999155600-A/36.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Michio,S., Takeshi,H., Masato,H. and Hideyuki,I.
TITLE Improved method for measuring cytokine gene expression
JOURNAL Patent: JP 1999155600-A 36 15-JUN-1999;
SHISEIDO CO LTD
COMMENT OS Unidentified
PN JP 1999155600-A/36
PD 15-JUN-1999
PF 28-NOV-1997 JP 1997328171
PR
PI MICHIIO SHIBATA,TAKESHI HARIYA,MASATO HATAO,HIDEYUKI ICHIKAWA
PC C1201/68,C07K14/52,C07K14/54,C07K14/55,C07K14/56,C07K14/57,PC
C12N15/09
PC G01N33/50/(C1201/68,C12R1:91)
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CC Topology: Linear;
FH Key
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Location/Qualifiers

FEATURES

source 1..22
Location/Qualifiers
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ORIGIN

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Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGACCTGCCAGGCGCCT 20
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Db 19 GGACCTGCCAGGCTCT 2

RESULT 12
AX292533
LOCUS AX292533 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 4295 from Patent WO0179548.
ACCESSION AX292533
VERSION AX292533.1 GI:17054216
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 4295 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source 1..24
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

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Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Db 7 GGACCTGGTAGTCTCT 24

RESULT 13
BD171375 21 bp DNA linear PAT 18-FEB-2003
LOCUS BD171375
DEFINITION Method for detecting bronchial asthma risk factor.
ACCESSION BD171375
VERSION BD171375.1 GI:28412665
KEYWORDS JP 2002218997-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 21)
AUTHORS Nakamura, Y. and Tamari, M.
TITLE Method for detecting bronchial asthma risk factor
JOURNAL Patent: JP 2002218997-A 10 06-AUG-2002;
OTSUKA PHARMACEUTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002218997-A/10
PD 06-AUG-2002
PF 25-JAN-2001 JP 2001017076
PI YUSUKE NAKAMURA, MAYUMI TAMARI
PC C1201/68, C12N15/09, C12N15/00
CC Primer sequence (FS) for PCR
FH Key Location/Qualifiers
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Location/Qualifiers
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/db_xref="taxon:32630"

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Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 ACCGCGCAGGCGCCT 20
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Db 5 ACCGCGCAGGCTTTT 20

RESULT 14
BD173609 21 bp DNA linear PAT 18-FEB-2003
LOCUS BD173609
DEFINITION Method of detecting bronchial asthma onset risk factor.
ACCESSION BD173609
VERSION BD173609.1 GI:28414940
KEYWORDS WO 02059305-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 21)
AUTHORS Nakamura, Y. and Tamari, M.
TITLE Method of detecting bronchial asthma onset risk factor
JOURNAL Patent: WO 02059305-A 10 01-AUG-2002;
OTSUKA PHARMACEUTICAL CO LTD, YUSUKE NAKAMURA, MAYUMI TAMARI
COMMENT OS Artificial Sequence
PN WO 02059305-A/10
PD 01-AUG-2002
PF 25-JAN-2002 WO 2002JP000540
PR 25-JAN-2001 JP 01P 017076
PI YUSUKE NAKAMURA, MAYUMI TAMARI
PC C12N15/12, C1201/68, G01N33/53
CC Primer sequence (FS) for PCR
FH Key Location/Qualifiers
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Db 5 ACCGCGCAGGCTTTT 20

RESULT 15
AX354409 22 bp DNA linear PAT 06-FEB-2002
LOCUS AX354409/c
DEFINITION Sequence 55 from Patent WO0196523.
ACCESSION AX354409
VERSION AX354409.1 GI:18619251
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1
AUTHORS Kennedy, G.C., Kang, S., Reinhard, C. and Jefferson, A.B.
TITLE Polynucleotides related to colon cancer
JOURNAL Patent: WO 0196523-A 55 20-DEC-2001;
CHIRON CORPORATION (US)
FEATURES
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Location/Qualifiers
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 Db 19 CCTCCAGTGTCTTT 4

Search completed: September 30, 2005, 11:34:58
 Job time : 1716 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: September 30, 2005, 09:06:54 ; Search time 415 Seconds
(without alignments)
299.553 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21
Sequence: 1 usgacugccagucgucut 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 1315584

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990a:.*
3: geneseqn2000a:.*
4: geneseqn2001a:.*
5: geneseqn2001b:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14.2	67.6	25	9	ACI63698
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7	13.8	65.7	25	9	ACI63698
8	13.8	65.7	25	9	ACI63698
9	13.8	65.7	29	10	ADK94415
10	13.8	65.7	29	10	ADK94415
11	13.6	64.8	26	6	ABK67185
12	13.6	64.8	26	6	ABK67185
13	13.6	64.8	28	10	AAH74915
14	13.4	63.8	25	2	AAH74915
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16	13.4	63.8	29	4	AAH74915
17	13.2	62.9	22	2	AAH74915
18	13.2	62.9	22	2	AAH74915
19	13.2	62.9	24	6	ABK67185
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27	12.8	61.0	25	13	AAH74915	AAH74915
28	12.8	61.0	26	10	AAH74915	AAH74915
29	12.8	61.0	26	10	AAH74915	AAH74915
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35	12.6	60.0	23	6	AAH74915	AAH74915
36	12.6	60.0	23	6	AAH74915	AAH74915
37	12.6	60.0	23	11	AAH74915	AAH74915
38	12.6	60.0	23	12	AAH74915	AAH74915
39	12.6	60.0	25	9	AAH74915	AAH74915
40	12.6	60.0	25	9	AAH74915	AAH74915
41	12.6	60.0	25	9	AAH74915	AAH74915
42	12.6	60.0	25	9	AAH74915	AAH74915
43	12.6	60.0	25	9	AAH74915	AAH74915
44	12.6	60.0	25	9	AAH74915	AAH74915
45	12.6	60.0	30	6	AAH74915	AAH74915

ALIGNMENTS

RESULT 1	AAH74915	AAH74915
ID	AAH74915	AAH74915
XX	AAH74915	AAH74915
AC	AAH74915	AAH74915
XX	AAH74915	AAH74915
DT	29-OCT-2001 (first entry)	
XX	29-OCT-2001 (first entry)	
DE	DNA sequence of encoded adaptor for detecting base 1 of template.	
XX	DNA sequence of encoded adaptor for detecting base 1 of template.	
KW	Nucleotide sequence signature; nucleotide sequencing; 86.	
OS	Synthetic.	
XX	MO200161044-A1.	
XX	23-AUG-2001.	
XX	15-FEB-2001; 2001WO-US05032.	
XX	15-FEB-2001; 2000US-0182454P.	
XX	01-SEP-2000; 2000US-0654187P.	
XX	(LYNX-) LYNX THERAPEUTICS INC.	
XX	Corcoran KC, Elter S;	
XX	WPI; 2001-522608/57.	
XX	Determining nucleotide sequence signature, by obtaining optical values	
XX	for each nucleotide position in a group, adjusting them to get ratio of	
XX	final highest values near predetermined factor, generating base call.	
XX	Disclosure; Page 15; 73pp; English.	
XX	The specification describes a method for determining a nucleotide	
XX	sequence signature. The method comprises obtaining optical measurements	
XX	with values indicating each nucleotide in a group of highest value	
XX	positions, adjusting the values until the ratio of highest value in the	
XX	set to next highest values in the set is at least a predetermined factor,	
XX	and generating a base call for a position in the group based on results	
XX	after the adjustment of values. The method is used for determining a	
XX	signature of a nucleotide sequence, and for determining a nucleotide	

CC sequence of a polynucleotide from a series of optical measurements.
 CC AAH74912-27 represent encoded adaptors, which are used for detecting
 CC bases of a DNA template, in the course of the invention
 XX

SO Sequence 28 BP; 4 A; 7 C; 7 G; 7 T; 0 U; 3 Other;

Query Match 69.5%; Score 14.6; DB 4; Length 28;
 Best Local Similarity 61.9%; Pred. No. 2.8e+03;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 UAGGACUCCAGUCUCUUTT 21
 Db 4 TACGAGCTGCAGTCCGCTTT 24

RESULT 2
 AC163698/C
 ID AC163698 standard; DNA; 25 BP.
 XX
 AC163698;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 63689.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (APFY-) APFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 63689; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used CC in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled CC compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly

CC from USPTO at seqdata.uspto.gov/sequence.html
 XX

SO Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 67.6%; Score 14.2; DB 9; Length 25;
 Best Local Similarity 63.2%; Pred. No. 4.3e+03;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGACUCCGAGUCUCUUTT 21
 Db 24 GGAAGTGAAGTGTCTTT 6

RESULT 3
 AAD51155
 ID AAD51155 standard; DNA; 28 BP.
 XX
 AC AAD51155;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Adapter DNA #10 used to illustrate the method of the invention.
 XX
 KW Genetic analysis; allelic analysis; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 4 /*tag= a
 FT /note= "Represented as X2 in the specification"
 FT
 XX
 PN WO200279496-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US009928.
 XX
 PR 28-MAR-2001; 2001US-00821694.
 XX
 PA (MIND-) APPLIED MINDS INC.
 XX
 PI Hillis WD;
 XX
 DR WPI; 2003-046825/04.
 XX
 PT Obtaining information on target nucleic acid analyte, by hybridizing
 PT target with oligonucleotide probes complementary, or complementary except
 PT at position of interest to target and analyzing probe hybridization.
 XX
 PS Example 1; Page 39; 66pp; English.

The invention relates to a method of obtaining information on a target CC nucleic acid analyte containing a target segment. The method involves CC hybridising target nucleic acid analyte with at least two oligonucleotide CC probes, where each probe comprises a sequence fully complementary, or CC complementary except at a position of interest or variable position, to CC the target nucleic acid analyte and analysing whether all, some or none CC of the probes hybridise. The method is useful for sequencing and for CC obtaining information on a number of target nucleic acid sequence CC segments, where information comprises the determination of a nucleotide CC at a position of interest. It is also useful for genetic or allelic CC analysis of genomic DNA or cDNA. The present sequence is an adapter DNA, CC used to illustrate the method of the invention

SO Sequence 28 BP; 4 A; 7 C; 7 G; 6 T; 0 U; 4 Other;

Query Match 67.6%; Score 14.2; DB 10; Length 28;
 Best Local Similarity 61.9%; Pred. No. 4.4e+03;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 UAGGACUCCAGUCUCUUTT 21
 : ||| : ||| : ||| : ||| : |||

DB		4 KACGAGCTGCAGTCGGCTTT 24
RESULT 4		
ID	ADP45901	
XX	ADP45901 standard; DNA; 30 BP.	
AC	ADP45901;	
DT	26-AUG-2004 (first entry)	
XX	PCR primer 4 used to genotype human MAP kinase MAPK10 polymorphism.	
KW	breast cancer; cytosstatic; gene therapy; human; ss; primer; PCR; SNP;	
KM	single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; p493F12;	
KV	p54bSAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;	
KW	c-Jun N-terminal kinase 3; stress activated protein kinase beta;	
KM	chromosome 4q22.1-q23.	
OS	Homo sapiens.	
PN	WO2004047623-A2.	
PD	10-JUN-2004.	
PF	25-NOV-2003; 2003WO-US037948.	
PR	25-NOV-2002; 2002US-0429136P.	
PR	24-JUL-2003; 2003US-0490234P.	
PA	(SEQU-) SEQUENOM INC.	
PI	Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;	
DR	WPI; 2004-441051/41.	
PT	Identifying a subject at risk of breast cancer by detecting the presence	
PT	of polymorphic variations in the ICAM, MAPK10, KIA00861, NMAL or GALE	
PT	regions which are associated with breast cancer in a nucleic acid sample	
PT	from a subject.	
PS	Example 5; Page 90; 28pp; English.	
CC	The invention relates to a novel method for identifying a subject at risk of	
CC	breast cancer comprising detecting the presence or absence of one or	
CC	more polymorphic variations associated with breast cancer in a nucleic	
CC	acid sample from a subject. The method of the invention has cytostatic	
CC	applications and may be useful for identifying a subject at risk of	
CC	breast cancer, for early diagnosis, prevention and treatment of breast	
CC	cancer, possibly via gene therapy, as well as to analyse and predict a	
CC	response to a breast cancer treatment and in clinical drug trials. The	
CC	current sequence is that of a PCR primer of the invention which was used	
CC	to genotype human MAP kinase MAPK10 (JNK3;JNK3A;p493F12;p54bSAPK MAP	
CC	kinase;c-jun kinase 3;JNK3 alpha protein kinase;c-jun N-terminal kinase 3	
CC	;stress activated protein kinase beta) gDNA which has been mapped to	
CC	chromosomal position 4q22.1-q23.	
SQ	Sequence 30 BP; 7 A; 6 C; 9 G; 8 T; 0 U; 0 Other;	
Query Match	67.6%; Score 14.2; DB 12; Length 30;	
Best Local Similarity	57.9%; Pred. No. 4.4e+03;	
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0		
OY	1 UAGGACUUCGCGAGUCGU 19	
Db	: : : : :	
	4 TTGGATGTGCCAGTCTCT 22	
RESULT 5		
ID	ADR94415	
XX	ADR94415 standard; DNA; 22 BP.	
AC	ADR94415;	

XX	06-MAY-2004	(first entry)
XX	Primer of the invention #135.	
XX	human; single nucleotide polymorphism; SNP; ss; primer.	
XX	Synthetic.	
XX	JP2003259875-A.	
XX	16-SEP-2003.	
XX	08-MAR-2002; 2002JP-00064373.	
XX	08-MAR-2002; 2002JP-00064373.	
XX	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.	
XX	WPI; 2004-093977/10.	
XX	Novel polynucleotide useful for PCR amplification along with two DNA	
XX	fragment from another set of sequences, or for detecting single	
XX	nucleotide polymorphism in human gene.	
XX	Claim 2; SEQ ID NO 3444; 2627bp; Japanese.	
XX	The present invention relates to a polynucleotide isolated from a human	
XX	gene and is useful for detecting a single nucleotide polymorphism in a	
XX	human gene or for diagnosing of disease. The invention enables the	
XX	detection of a single nucleotide polymorphism in a human gene. The	
XX	present sequence represents a primer of the invention.	
XX	Sequence 22 BP; 3 A; 7 C; 5 G; 7 T; 0 U; 0 Other;	
XX	Query Match	65.7%; Score 13.8; DB 12; Length 22;
XX	Best Local Similarity	64.7%; Pred. No. 6.7e+03;
XX	Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;	
OY	1 UAGACCCUGCCAGUGCU 17	
	: : :	
DB	4 TAGACTCTTCACGTGCT 20	
RESULT 6		
AAD02074/c		
ID	AAD02074 standard; DNA; 23 BP.	
XX	AAD02074;	
XX	26-MAR-2001 (first entry)	
DE	3' PCR primer for preparing N-myc fusion construct.	
KM	Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;	
KM	TNF-receptor associated factor; TRAF2 truncated; TRAF2TR; TRAF2TD;	
KM	TRAF2 truncated-deleted; antiinflammatory; cardiant; Myc tag; vasotropic;	
KM	antiproliferic; antihemetic; antiarthritic; antidiabetic;	
KM	antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;	
KM	rheumatoid arthritis; graft versus host disease; cardiovascular disease;	
KM	non-insulin dependent diabetes; inflammatory bowel disease; stroke;	
KM	neurodegenerative disease; congestive heart failure; PCR primer;	
KM	myocardial infarction; nuclear factor kappa B; NFkB; ss.	
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO20006737-A1.	
XX	09-NOV-2000.	
PF	06-APR-2000; 2000MO-US009178.	

PR 30-APR-1999; 99US-0131940P.
XX (AVET) AVENTIS PHARM PROD INC.
XX
XX
PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX MPI; 2001-007223/01.
XX
XX
XX New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
XX rheumatoid arthritis.
XX
XX Example 3; Page 42; 74pp; English.
XX
XX The present invention relates to variants of tumour necrosis factor (TNF)
CC -receptor associated factor (TRAF2). TRAF2 has two variants, a splice
CC variant referred as "TRAF2 truncated" (TRAF2TR) and an expression
CC construct with enhanced dominant negative properties referred as "TRAF2
CC truncated-deleted" (TRAF2TD). TRAF2 variants are capable of inhibiting
CC TNF alpha signalling pathways and for inhibiting diseases involving over
CC production of TNFalpha, TNFalpha pathologies involving hyperactivation of
CC nuclear factor kappa B (NFkB). The variants are also useful for
CC inhibiting and treating inflammatory processes involving TNFalpha such as
CC Crohn's disease, psoriasis, rheumatoid arthritis, graft versus host
CC disease, non-insulin dependent diabetes, inflammatory bowel disease, and
CC neurodegenerative diseases or cardiovascular diseases such as cardiac
CC ischaemia-reperfusion injury following myocardial infarction, coronary
CC artery bypass surgery, cardiac transplantation or ischaemia-reperfusion
CC injury in the central nervous system (CNS) following stroke, the
CC progression and rupture of advanced coronary atherosclerotic plaques,
CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells. The present sequence is a 3' PCR primer for preparing a
CC fusion construct containing N-myc affinity tag as well as truncated and
CC full length TRAF2. N-myc is useful for determining the effect of TRAF2TR
CC on NFkB activation. Truncated as well as full length TRAF2 were
CC constructed with N-myc affinity tags in a mammalian expression vector
CC (pCDNA3). N-myc fusion constructs were prepared using 5' and 3' PCR
XX primers
XX
SQ Sequence 23 BP; 6 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 65.7%; Score 13.8; DB 5; Length 23;
Best Local Similarity 70.6%; Pred. No. 6.7e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 3 GGACCGCCAGGCGUCU 19
Db 19 GGACCTGACGAGGCTCT 3
|||:|||||:|:
ACCK21937/c
ID ACK21937 standard; DNA; 25 BP.
XX
XX ACK21937;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 121918.
DE
XX EST; sg; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX PD
XX PF 15-MAR-2002; 2002US-00098263.
XX
XX

XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX
XX Miltmann MP;
XX MPI; 2003-567953/53.
XX
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX
XX Claim 1; SEQ ID NO 121918; 9pp; English.
XX
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termin of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX
SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 65.7%; Score 13.8; DB 9; Length 25;
Best Local Similarity 70.6%; Pred. No. 6.8e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 4 GACCGCCAGGCGUCUT 20
Db 21 GACCTGCGCAGACTCTT 5
|||:|||||:|:
ACIS8170/c
ID ACIS8170 standard; DNA; 25 BP.
XX
XX ACIS8170;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 58161.
DE
XX EST; sg; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX PF
XX PR 16-MAR-2001; 2001US-0276759P.
XX
XX

XX (AFY-) AFFYMETRIX INC.
 PA Miltmann MP;
 XX WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 58161; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 65.7%; Score 13.8; DB 9; Length 25;
 Best Local Similarity 70.6%; Pred. No. 6.8e+03;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 5 ACCGCGCAGGCGCCTT 21
 Db 25 ACCAGCCAGTGTCTT 9
 Db
 RESULT 9
 ADCA7044
 ID ADCA7044 standard; DNA; 29 BP.
 AC ADCA7044;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE BEC1 potassium channel inhibitor related primer #SEQ ID 6.
 XX
 KW BEC1 potassium channel inhibitor; nootropic; neuroprotective;
 KW brain-specific eag-like channel 1; dementia; learning disability;
 KW inhibitor; PCR; primer; ss.
 XX
 OS Synthetic.
 OS
 PN WO2003066099-A1.
 PD 14-AUG-2003.
 PF 03-FEB-2003; 2003WO-JP001065.
 PR 05-FEB-2002; 2002JP-00028844.
 PA (YAMA) YAMANOUCHI PHARM CO LTD.

XX Kubota H, Suzuki T, Miura M, Nakai E, Yabiro K, Miyake A;
 PI Mochizuki S, Nakatou K;
 XX
 DR WPI; 2003-697418/56.
 XX
 PT Antidementia agents comprise new and known brain-specific eag-like
 PT channel 1 (BEC1) potassium channel inhibitors.
 XX
 PS Disclosure; Page 90; 95pp; Japanese.
 XX
 CC The invention relates to an antidementia agent that comprises a brain-
 CC specific eag-like channel 1 (BEC1) potassium channel inhibitor. Agents of
 CC the invention are used as BEC1 potassium channel inhibitors for creating
 CC and preventing dementia and learning disabilities. The current sequence
 CC represents the BEC1 potassium channel inhibitor related PCR primer
 CC sequence.
 XX
 SQ Sequence 29 BP; 3 A; 11 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 65.7%; Score 13.8; DB 10; Length 29;
 Best Local Similarity 70.6%; Pred. No. 6.9e+03;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 4 GACCTGCCAGGCGCCTT 20
 Db 8 GACCTGCCAGGCGCCTT 24
 Db
 RESULT 10
 ADI35763
 ID ADI35763 standard; DNA; 29 BP.
 XX
 AC ADI35763;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human potassium channel protein BEC1 related PCR primer SEQ ID NO:6.
 XX
 KW transgenic animal; potassium channel; BEC1; nootropic; tranquilliser;
 KW dementia; memory loss; anxiety; learning ability; human; PCR; ss; primer.
 OS Homo sapiens.
 OS Synthetic.
 PN WO2003041496-A1.
 PD 22-MAY-2003.
 PF 13-NOV-2002; 2002WO-JP011843.
 PR 14-NOV-2001; 2001JP-00349286.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA
 PI Miyake A, Nakamura Y, Ni J, Mochizuki S;
 XX
 DR WPI; 2003-457459/43.
 XX
 PT Transgenic animal overexpressing potassium channel BEC1 for
 PT screening potential treatments for dementia and anxiety.
 XX
 PS Example 1; SEQ ID NO 6; 56pp; Japanese.
 XX
 CC The present invention describes a transgenic animal transformed by a
 CC promoter together with a polynucleotide encoding potassium channel
 CC protein BEC1 or encoding a protein derived from BEC1 by addition,
 CC deletion and/or substitution of up to ten amino acid residues and at
 CC least 90% homologous to it. Also described: (1) screening (M1) for
 CC substances for the treatment of dementia, memory loss and anxiety using
 CC the transgenic animal as a disease model; and (2) the preparation (M2) of
 CC drug compositions containing as active components substances identified
 CC by (M1). BEC1 has nootropic and tranquilliser activities. The transgenic

Query Match 64.8%; Score 13.6; DB 6; Length 26;
 Best Local Similarity 65.0%; Pred. No. 8.5e+03;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGGACCTGCGACGUCUCUTT 21
 |||||:||||:|:
 DB 4 AGGACCTTCCAGTCTTACTT 23

RESULT 13

AD51147
 ID AD51147 standard; DNA; 28 BP.

AC AAD51147;

DT 02-APR-2003 (first entry)

DE Adapter DNA #2 used to illustrate the method of the invention.

XX Genetic analysis; allelic analysis; ss.

OS Unidentified.

XX Key Location/Qualifiers

FT modified_base 4 /*tag= a

FT /mod_base= OTHER

FT /note= "8-oxo-dG"

XX MO200279496-A2.

XX 10-OCT-2002.

XX 27-MAR-2002; 2002MO-US009928.

XX 28-MAR-2001; 2001US-00821694.

XX (MIND-) APPLIED MINDS INC.

XX H1111s WD;

XX WPI; 2003-046825/04.

XX Obtaining information on target nucleic acid analyte, by hybridizing

XX target with oligonucleotide probes complementary, or complementary except

XX at position of interest to target and analyzing probe hybridization.

XX Example 1; Page 39; 66pp; English.

XX The invention relates to a method of obtaining information on a target

XX nucleic acid analyte containing a target segment. The method involves

XX hybridizing target nucleic acid analyte with at least two oligonucleotide

XX probes, where each probe comprises a sequence fully complementary, or

XX complementary except at a position of interest or variable position, to

XX the target nucleic acid analyte and analyzing whether all, some or none

XX of the probes hybridize. The method is useful for sequencing and for

XX obtaining information on a number of target nucleic acid sequence

XX segments, where information comprises the determination of a nucleotide

XX at a position of interest. It is also useful for genetic or allelic

XX analysis of genomic DNA or cDNA. The present sequence is an adapter DNA,

XX used to illustrate the method of the invention

XX Sequence 28 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 3 Other;

XX Query Match 64.8%; Score 13.6; DB 10; Length 28;

XX Best Local Similarity 65.0%; Pred. No. 8.6e+03;

XX Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGGACCTGCGACGUCUCUTT 21
 |||||:|||||:|:
 DB 5 ACAGCTGCCAGTCCGCTTT 24

RESULT 14
 AAT32267
 ID AAT32267 standard; DNA; 25 BP.

XX AAT32267;

XX 07-JAN-1997 (first entry)

DE Probe for the detection of lesions associated with neoplastic cells.

XX Probe; detection; lesion; neoplasia; neoplastic cells; cancer; prognosis;

XX therapy; tumour cell; tumour; homozygous loss; ss.

XX Synthetic.

XX WO9619589-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95MO-US016766.

XX 20-DEC-1994; 94US-00360096.

XX (COLD-) COLD SPRING HARBOR LAB.

XX Wiggler M, Lisitsyn N;

XX WPI; 1996-309603/31.

XX Nucleic acid sequence probes - are used for the detection of lesions

XX associated with neoplastic cells.

XX Claim 1; Page 23; 31pp; English.

XX The nucleic acid sequence probes described in AAT32244-78 are used for

XX the detection of lesions associated with neoplastic cells. The sequences

XX can be used for identifying the locus associated with the lesion, for

XX determining cancer susceptibility of cells, as well as categorising and

XX characterising tumour cells for prognosis and therapy. Two probes

XX (AAT32267, AAT32268) were used to detect homozygous loss in tumour cell

XX lines at chromosome location 18

XX Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

XX Query Match 63.8%; Score 13.4; DB 2; Length 25;

XX Best Local Similarity 73.3%; Pred. No. 1.1e+04;

XX Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 UNAGACCTGCGACGUG 15
 :|||||:|||||:
 DB 3 TAGGACTGCCAGTG 17

RESULT 15
 AAT71677
 ID AAT71677 standard; DNA; 25 BP.

XX AAT71677;

XX 04-FEB-1998 (first entry)

DE Cancer detection probe VAKO441-9 PCR 5' primer.

XX PCR primer; VAKO441-9; detection; neoplastic; lesion; tumour; RDA;

XX homozygous loss; representational difference analysis; probe; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9722721-A2.

XX 26-JUN-1997.

```

PF 20-DEC-1996; 96WO-US020631.
XX
XX 21-DEC-1995; 95US-00576202.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Wiegler M, Lisitsyn N;
XX
XX WPI; 1997-341709/31.
XX
XX
XX New cancer detection probes - useful for detecting genomic lesions
XX associated with neoplasia in human cells, e.g. for detection, prognosis
XX and therapy of cancer.
XX
XX Claim 10; Page 23; 32pp; English.
XX
XX This primer is used to amplify a PCR product of 244 bp used as a probe in
XX a standard PCR panel for determination of a lesion associated with
XX neoplasia in human cells. In particular, this probe identifies a
XX homozygous loss in tumour cell line at chromosome location 18. The DNA
XX can be obtained by standard representational difference analysis (RDA).
XX RDA was performed using Bgl II restriction endonuclease on tumour DNA
XX (driver) and matched with normal DNA (tester). Pure tumour DNAs of the
XX RDA difference products were cloned into plasmids. Selected plasmid
XX inserts were analysed by Southern blot hybridisation. Oligonucleotides
XX synthesised from selected plasmid insert sequences were used to screen a
XX standard PCR panel of DNAs from tumour cell lines and a control DNA.
XX Probes were subsequently mapped to human chromosomes by PCR using an
XX existing panel of human rodent somatic cell hybrids. The DNA can be used
XX for detecting genomic lesions associated with cancer and for prognosis
XX and therapy. The DNA sequences can also be used to obtain other suitable
XX probes by walking genomic DNA to obtain a secondary probe, and repeating
XX the walking to obtain successive probes which are screened with normal
XX and tumour cells
XX
XX
XX SQ Sequence 25 BP; 5 A; 5 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 63.8%; Score 13.4; DB 2; Length 25;
XX Best Local Similarity 73.3%; Pred. No. 1.1e+04;
XX Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 UAGGACCCGCGCAGUG 15
XX : ||||| : ||||| : |
XX
XX Db 3 TAGGAACCTGCCAGTG 17

```

Search completed: September 30, 2005, 09:14:08
 Job time : 421 sec8

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using bw model

Run on: September 30, 2005, 09:06:54 ; Search time 123 Seconds
(without alignments)
279.364 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21
Sequence: 1 usgacugcagucgucucut 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 569154

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	75.2	25	4	US-09-396-196G-107545, Sequence 107545, A
2	14.8	70.5	25	4	US-09-396-196G-40269, Sequence 40269, A
3	14.8	70.5	25	4	US-09-396-196G-55195, Sequence 55195, A
4	14.8	70.5	25	4	US-09-396-196G-55196, Sequence 55196, A
5	14.4	68.6	25	4	US-09-396-196G-48277, Sequence 48277, A
6	14.4	68.6	25	4	US-09-396-196G-107546, Sequence 107546, A
7	14	66.7	25	4	US-09-396-196G-48278, Sequence 48278, A
8	14	66.7	25	4	US-09-396-196G-52121, Sequence 52121, A
9	14	66.7	25	4	US-09-396-196G-52122, Sequence 52122, A
10	13.6	64.8	26	2	US-08-859-998-1273, Sequence 1273, Ap
11	13.6	64.8	26	2	US-08-859-998-1273, Sequence 1273, Ap
12	13.6	64.8	26	3	US-09-396-196G-1273, Sequence 1273, Ap
13	13.6	64.8	26	3	US-09-396-196G-1273, Sequence 1273, Ap
14	13.6	64.8	26	4	US-09-396-196G-1273, Sequence 1273, Ap
15	13.6	64.8	26	4	US-09-396-196G-1273, Sequence 1273, Ap
16	13.4	63.8	25	1	US-08-373-737A-12, Sequence 12, Ap
17	13.4	63.8	25	1	US-08-373-737A-12, Sequence 12, Ap
18	13.4	63.8	25	3	US-08-576-202-24, Sequence 24, Ap
19	13.4	63.8	25	4	US-09-396-196G-48276, Sequence 48276, A
20	13.4	63.8	25	4	US-09-396-196G-113766, Sequence 113766, A
21	13.4	63.8	25	4	US-09-396-196G-113766, Sequence 113766, A
22	13.4	63.8	25	5	PCR-US95-16766-24, Sequence 24, Ap
23	13.2	62.9	25	4	US-09-396-196G-18422, Sequence 18422, A
24	13.2	62.9	25	4	US-09-396-196G-18423, Sequence 18423, A
25	13.2	62.9	25	4	US-09-396-196G-18423, Sequence 18423, A
26	13.2	62.9	25	4	US-09-396-196G-66673, Sequence 66673, A
27	13.2	62.9	25	4	US-09-396-196G-66674, Sequence 66674, A

28	13.2	62.9	25	4	US-09-396-196G-122627, Sequence 122627, A
29	13	61.9	25	4	US-09-396-196G-107084, Sequence 107084, A
30	12.8	61.0	25	4	US-09-396-196G-5116, Sequence 5116, Ap
31	12.8	61.0	25	4	US-09-396-196G-62374, Sequence 62374, A
32	12.8	61.0	25	4	US-09-396-196G-68909, Sequence 68909, A
33	12.8	61.0	25	4	US-09-396-196G-81723, Sequence 81723, A
34	12.8	61.0	25	4	US-09-396-196G-107544, Sequence 107544, A
35	12.6	60.0	25	4	US-09-396-196G-14106, Sequence 14106, A
36	12.6	60.0	25	4	US-09-396-196G-64352, Sequence 64352, A
37	12.6	60.0	25	4	US-09-396-196G-64353, Sequence 64353, A
38	12.6	60.0	25	4	US-09-396-196G-91219, Sequence 91219, A
39	12.6	60.0	25	4	US-09-396-196G-91220, Sequence 91220, A
40	12.6	60.0	25	4	US-09-396-196G-93099, Sequence 93099, A
41	12.6	60.0	25	4	US-09-396-196G-113638, Sequence 113638, A
42	12.6	60.0	25	4	US-09-396-196G-113639, Sequence 113639, A
43	12.6	60.0	30	2	US-08-859-998-1260, Sequence 1260, Ap
44	12.6	60.0	30	3	US-09-396-196G-1260, Sequence 1260, Ap
45	12.6	60.0	30	4	US-09-225-201B-1260, Sequence 1260, Ap

ALIGNMENTS

```

RESULT 1
US-09-396-196G-107545
; Sequence 107545, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107545

Query Match      75.2%; Score 15.8; DB 4; Length 25;
Best Local Similarity 68.4%; Pred. No. 1.9e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2  AGAGCCUGCCAGUCUCUCUT 20
Db      1  AAGAGCTGCCAGTCTCTT 19

RESULT 2
US-09-396-196G-40269
; Sequence 40269, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affimetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40269

```

LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-40269

Query Match 70.5%; Score 14.8; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGACCCGCGAGUCGUC 18
|:|:|:|:|:|:|:|:|:|:
DB 2 TAGGAAGTCCAGTGTTC 19

RESULT 3
US-09-396-196G-55195
Sequence 55195, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55195

LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus
US-09-396-196G-55195

Query Match 70.5%; Score 14.8; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCGCCGAGUCGUCUTT 21
|:|:|:|:|:|:|:|:|:|:
DB 7 GAGTGCCTGTGCTCTTT 24

RESULT 4
US-09-396-196G-55196
Sequence 55196, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55196

LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-55196

Query Match 70.5%; Score 14.8; DB 4; Length 25;
Best Local Similarity 66.7%; Pred. No. 5.9e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCGCCGAGUCGUCUTT 21
|:|:|:|:|:|:|:|:|:|:
DB 1 GAGTGCCTGTGCTCTTT 18

RESULT 5
US-09-396-196G-48277
Sequence 48277, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48277

LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus
US-09-396-196G-48277

Query Match 68.6%; Score 14.4; DB 4; Length 25;
Best Local Similarity 68.8%; Pred. No. 9.2e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUCGUCUTT 20
|:|:|:|:|:|:|:|:|:|:
DB 2 AACTGCCAGTGTCTTT 17

RESULT 6
US-09-396-196G-107546
Sequence 107546, Application US/09396196G
Patent No. 6821724

GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 107546

LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus
US-09-396-196G-107546

Query Match 68.6%; Score 14.4; DB 4; Length 25;
Best Local Similarity 68.8%; Pred. No. 9.2e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACCUGCCAGUCGUCUTT 20
|:|:|:|:|:|:|:|:|:|:
DB 1 AGCTGCCAGTGTCTTT 16

RESULT 7
US-09-396-196G-48278
Sequence 48278, Application US/09396196G
Patent No. 6821724

```

; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-48278
```

```

Query Match          66.7%; Score 14; DB 4; Length 25;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7  CUGCCAGUGCUCUT 20
Db      1  CTGCCAGTGTCTT 14
```

```

RESULT 8
US-09-396-196G-52121/c
; Sequence 52121, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52121
```

```

Query Match          66.7%; Score 14; DB 4; Length 25;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7  CUGCCAGUGCUCUT 20
Db      21 CTGCCAGTGTCTT 8
```

```

RESULT 9
US-09-396-196G-52122/c
; Sequence 52122, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
```

```

; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-52122
```

```

Query Match          66.7%; Score 14; DB 4; Length 25;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7  CUGCCAGUGCUCUT 20
Db      18 CTGCCAGTGTCTT 5
```

```

RESULT 10
US-08-859-998-1273/c
; Sequence 1273, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Johhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 1273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1273
```

```

Query Match          64.8%; Score 13.6; DB 2; Length 26;
Best Local Similarity 55.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  UAGGACCCGCGAGUCUCUT 20
          : ||| | : ||| | : ||| | :
```

Db 20 TTGGCCTTCCGGTGCTCTT 1

RESULT 11
US-08-859-998-1326
Sequence 1326, Application US/0885998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1326:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1326

Query Match 64.8%; Score 13.6; DB 2; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCTTCCAGTCTCTT 21
Db 4 AGGACCTTCCAGTCTCTT 23

RESULT 12
US-09-225-928-1273/C
Sequence 1273, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

Qy 1 UNGACCTGCGGAGTCTCTT 20
Db 20 TTGGCCTTCCGGTGCTCTT 1

RESULT 13
US-09-225-928-1273
Sequence 1326, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1326:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-928-1326

Query Match 64.8%; Score 13.6; DB 3; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGGCGCCTT 21
|||||:||||:|
Db 4 AGGACCTTCAGTCTACTT 23

RESULT 14
US-09-225-201B-1273/c
Sequence 1273, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilahevili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1273:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1273:
US-09-225-201B-1273

Query Match 64.8%; Score 13.6; DB 4; Length 26;
Best Local Similarity 55.0%; Pred. No. 2.3e+03;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 UAGACCGCCAGGCGCCTT 20
:|||||:||||:|
Db 20 TTGACCTTCAGTCTACTT 1

RESULT 15
US-09-225-201B-1326
Sequence 1326, Application US/09225201B
Patent No. 6489455
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilahevili, Robert

TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,201B
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.

REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1326:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA
FEATURE:

OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1326:
US-09-225-201B-1326

Query Match 64.8%; Score 13.6; DB 4; Length 26;
Best Local Similarity 65.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGGACCGCCAGGCGCCTT 21
|||||:||||:|
Db 4 AGGACCTTCAGTCTACTT 23

Search completed: September 30, 2005, 11:06:11
Job time : 124 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: September 30, 2005, 09:06:54 ; Search time 3585 Seconds
(without alignments)
40.446 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usgaccugccagucucuc 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 6109502

Minimum DB seq length: 21

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/PCRUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
19: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
20: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
21: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
22: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq:*
24: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	25	22	US-10-738-413-1
2	15.8	75.2	25	21	US-10-809-189-107545
3	15.2	72.4	25	21	US-10-719-900-424586
4	14.8	70.5	25	21	US-10-809-189-40269
5	14.8	70.5	25	21	US-10-809-189-55195
6	14.8	70.5	25	21	US-10-809-189-55196
7	14.8	70.5	25	21	US-10-956-157-154607

8	14.8	70.5	25	22	US-10-719-956-560046	Sequence 560046,
9	14.8	70.5	25	22	US-10-719-956-560047	Sequence 560047,
10	14.6	69.5	28	17	US-10-407-089-5	Sequence 5, Appl1
11	14.4	68.6	25	21	US-10-719-900-355242	Sequence 355242,
12	14.4	68.6	25	21	US-10-719-900-725466	Sequence 725466,
13	14.4	68.6	25	21	US-10-719-900-867852	Sequence 867852,
14	14.4	68.6	25	21	US-10-719-900-861525	Sequence 861525,
15	14.4	68.6	25	21	US-10-809-189-48277	Sequence 48277, A
16	14.4	68.6	25	21	US-10-809-189-107546	Sequence 107546,
17	14.4	68.6	25	22	US-10-719-956-35641	Sequence 35641, A
18	14.4	68.6	25	22	US-10-719-956-475341	Sequence 475341,
19	14.4	68.6	25	22	US-10-719-956-475343	Sequence 475343,
20	14.2	67.6	25	15	US-10-098-2638-63689	Sequence 63689, A
21	14.2	67.6	25	21	US-10-719-900-59543	Sequence 59543, A
22	14.2	67.6	25	21	US-10-719-900-145845	Sequence 145845,
23	14.2	67.6	25	21	US-10-719-900-436263	Sequence 436263,
24	14.2	67.6	25	21	US-10-719-900-477557	Sequence 477557,
25	14.2	67.6	25	21	US-10-719-900-485539	Sequence 485539,
26	14.2	67.6	25	21	US-10-719-900-787669	Sequence 787669,
27	14.2	67.6	25	22	US-10-719-956-34410	Sequence 34410, A
28	14.2	67.6	25	22	US-10-719-956-44564	Sequence 44564, A
29	14.2	67.6	25	22	US-10-719-956-139996	Sequence 139996,
30	14.2	67.6	25	22	US-10-719-956-152482	Sequence 152482,
31	14.2	67.6	25	22	US-10-719-956-156015	Sequence 156015,
32	14.2	67.6	25	22	US-10-719-956-156350	Sequence 156350,
33	14.2	67.6	28	11	US-09-821-694A-16	Sequence 16, Appl1
34	14.2	67.6	28	10	US-09-821-694A-16	Sequence 16, Appl1
35	14.2	67.6	30	22	US-10-723-681-321	Sequence 321, App
36	14	66.7	25	21	US-10-719-900-455910	Sequence 455910,
37	14	66.7	25	21	US-10-719-900-589497	Sequence 589497,
38	14	66.7	25	21	US-10-719-900-655445	Sequence 655445,
39	14	66.7	25	21	US-10-809-189-48278	Sequence 48278, A
40	14	66.7	25	21	US-10-809-189-52121	Sequence 52121, A
41	14	66.7	25	21	US-10-809-189-52122	Sequence 52122, A
42	13.8	65.7	25	15	US-10-098-2638-58161	Sequence 58161, A
43	13.8	65.7	25	15	US-10-098-2638-121918	Sequence 121918,
44	13.8	65.7	25	21	US-10-719-900-580044	Sequence 580044, A
45	13.8	65.7	25	21	US-10-719-900-118070	Sequence 118070,

ALIGNMENTS

RESULT 1
US-10-738-413-1
; Sequence 1, Application US/10738413
; Publication No. US20050137151A1
; GENERAL INFORMATION:
; APPLICANT: BINETTI, RALPH R.
; TITLE OF INVENTION: SI-RNA-MEDIATED GENE SILENCING TECHNOLOGY TO INHIBIT
; FILE REFERENCE: SC66U-US
; CURRENT APPLICATION NUMBER: US/10/738,413
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-738-413-1

Query Match 100.0%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGGACUCCAGUCUCUUTT 21
Db 1 UAGGACUCCAGUCUCUUTT 21

RESULT 2

US-10-809-189-107545
; Sequence 107545, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-107545

Query Match 75.2%; Score 15.8; DB 21; Length 25;
Best Local Similarity 68.4%; Pred. No. 4.6e+02;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGACUCCAGUCUCUUTT 20
Db 1 AAGAGCTGCCAGTGTCTTT 19

RESULT 3

US-10-719-900-424586/C
; Sequence 424586, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 424586
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-424586

Query Match 72.4%; Score 15.2; DB 21; Length 25;
Best Local Similarity 60.0%; Pred. No. 9.4e+02;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 UAGGACUCCAGUCUCUUTT 20
Db 21 TTGGACCTGCCAGTATCTT 2

RESULT 4
US-10-809-189-40269
; Sequence 40269, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40269
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-40269

Query Match 70.5%; Score 14.8; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 UAGGACUCCAGUCUCUUTT 18
Db 2 TAGGAAGTCCAGTGTCTT 19

RESULT 5

US-10-809-189-55195
; Sequence 55195, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55195
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-55195

Query Match 70.5%; Score 14.8; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAGCUGCCAGUCUCUUTT 21
Db 7 GAGCTGCTGTGTCTTT 24

RESULT 6

US-10-809-189-55196
; Sequence 55196, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55196
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-10-809-189-55196

Query Match 70.5%; Score 14.8; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 GACCCGACGAGCUCU 21
DB 1 GAGCTGCTGTGCTCTT 18

RESULT 7
US-10-956-157-154607

Sequence 154607, Application US/10956157
Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

FILE REFERENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: PatentIn version 3.2

SEQ ID NO 154607

LENGTH: 25

TYPE: DNA

ORGANISM: Probe Sequence

US-10-956-157-154607

Query Match 70.5%; Score 14.8; DB 21; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGGACCCGACGAGCUCU 19
DB 4 AGGATCTGACAGTCTCTT 21

RESULT 8

US-10-719-956-560046

Sequence 560046, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 560046

LENGTH: 25

TYPE: DNA

ORGANISM: Rattus norvegicus

US-10-719-956-560046

Query Match 70.5%; Score 14.8; DB 22; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGACCCGACGAGCUC 18
DB 1 TAGGACCTGACATGCTC 18

RESULT 9

US-10-719-956-560047

Sequence 560047, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 560047

LENGTH: 25

TYPE: DNA

ORGANISM: Rattus norvegicus

US-10-719-956-560047

Query Match 70.5%; Score 14.8; DB 22; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAGACCCGACGAGCUC 18
DB 1 TAGGACCTGACATGCTC 18

RESULT 10

US-10-407-089-5

Sequence 5, Application US/10407089

Publication No. US20030224419A1

GENERAL INFORMATION:

APPLICANT: Corcoran, Kevin C.

TITLE OF INVENTION: System for Determining a Signature of a

FILE REFERENCE: 55525-8040-US00

CURRENT APPLICATION NUMBER: US/10/407,089

CURRENT FILING DATE: 2003-04-02

PRIOR APPLICATION NUMBER: US/09/654,187

PRIOR FILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: US 60/182,454

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: PCT/US98/11224

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: US 08/862,610

PRIOR FILING DATE: 1997-05-23

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: encoded adaptor

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(28)

OTHER INFORMATION: n = A,T,C or G

US-10-407-089-5

Query Match 69.5%; Score 14.6; DB 17; Length 28;

Best Local Similarity	61.9%	Pred. No. 1.9e+03:	
Matches	13;	Conservative	4; Mismatches 4; Indels 0; Gaps 0;
Oy	1 UAGAGACCTGCGACGUCUCUTT	21	
	: : : : : : : : : : :		
Db	4 TACGAGCTGCCAGTCCGCTTT	24	

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RESULT 11
US-10-719-900-355242
; Sequence 355242, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Lactating Genator V 1.1.1
; SEQ ID NO 355242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-355242

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Query Match	68.6%	Score 14.4	DB 21	Length 25
Best Local Similarity	68.8%	Pred. No. 2.4e+03		
Matches	11	Conservative	4	Mismatches 1
				Indels 0
				Gaps 0
Oy	6	CCUGCCAGUCUCUUTT	21	
		: : : :		
Ob	1	CCGCGACATCCUUTT	16	

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RESULT 12
US-10-719-900-726466/c
; Sequence 726466, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 726466
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-726466

```

Query Match	68.6%	Score 14.4	DB 21	Length 25
Best Local Similarity	75.0%	Pred. No. 2.4e+03		
Matches	12	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
QY	2	AGGACUCGSCAAGUCU	17	
db	25	AGTACCTGCGCAGTCT	10	

RESULT 13
US-10-719-900-867852/c
; Sequence 867852, Application US/10719900
; Publication No. US2005002616A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mice

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; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 867852
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-867852

Query Match      68.6%; Score 14.4; DB 21; Length 25;
Best Local Similarity 81.2%; Pred. No. 2.4e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 UAGACCTGCCAGUGC 16
: |||||: |||||
Db 17 TAGACCTGCCAGGCG 2

```

RESULT 14
US-10-719-900-961525
; Sequence 961525, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1.
; SEQ ID NO 961525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-961525

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Query Match	68.6%	Score 14.4	DB 21	Length 25
Best Local Similarity	75.0%	Pred. No. 2.4e+03		
Matches 12, Conservative	3	Mismatches 1	Indels 0	Gaps 0
OY	2	AGGACCTGGCCAGGCGCU	17	
Db	8	AGGAGCTGCCAGTGCT	23	

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/ RESULT 15
/ US-10-809-189-48277
/ Sequence 48277, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mitcman
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 48277
/
/ LENGTH: 25
/ TYPE: DNA
/

```

; ORGANISM: mus musculus
 US-10-809-189-48277

Query Match 68.64; Score 14.4; DB 21; Length 25;
 Best Local Similarity 68.84; Pred. No. 2.4e+03;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Caps 0;

QY 5 ACCUGCCAGUGCUCUT 20
 |:||:||:||:||:
 Db 2 AACTGCCAGTGTCTT 17

Search completed: September 30, 2005, 10:13:59
 Job time : 3585 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: September 30, 2005, 09:06:54 ; Search time 2985 Seconds
(without alignments)
267.789 Million cell updates/sec

Title: US-10-738-413-1

Perfect score: 21

Sequence: 1 usgaccugccagucucut 21

Scoring table: IDENTITY_NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 34436

Minimum DB seq length: 21
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.6	60.0	30	9	CL982942 GC0170 T1
2	12.2	58.1	28	8	AZ821702 2M0094001
3	12.2	58.1	28	9	AG192441 Pan trogl
4	11.6	55.2	28	1	AI370776 qz89c10.x
5	11.6	52.4	22	9	AJ592231 Arabidops
6	11.6	52.4	29	8	AZ847949 2M0148B23
7	10.8	51.4	26	8	AZ815857 2M0084A01
8	10.6	50.5	24	8	AZ617463 1M0448P15
9	10.4	49.5	28	1	AL042578 DKFZP434J
10	10.4	49.5	28	8	AZ642513 1M0505N01
11	10.4	49.5	29	8	AZ454477 1M0256N22
12	10.4	49.5	30	4	BG424013 602447475
13	10.2	48.6	22	8	AZ603158 1M0422L13
14	10.2	48.6	28	1	AA937308 cm16h06.8
15	10.2	48.6	28	9	AB004341 Mouse gen
16	10.2	48.6	29	8	AZ315608 1M003G223
17	10.2	48.6	29	8	AZ618039 1M0449004
18	10.2	48.6	29	8	AZ663335 1M0542J20
19	10.2	47.6	22	8	AZ324102 1M0045H23
20	10.2	47.6	22	8	AZ345644 1M0080J22
21	10.2	47.6	23	8	AZ58148 T. brucei
22	10.2	47.6	24	9	CL666753 PR10153b
23	10.2	47.6	25	9	AL481946 T. brucei
24	10.2	47.6	26	1	AJ747615 AJ747615

C 25	10	47.6	26	9	CG721091	CG721091 1119065D0
C 26	10	47.6	27	8	AZ329457	AZ329457 1M0053P08
C 27	10	47.6	27	9	CG723351	CG723351 1119076A0
C 28	10	47.6	29	7	CF292082	CF292082 14ROOT--0
C 29	10	47.6	29	7	CF295445	CF295445 30DGS--05
C 30	10	47.6	29	7	CF295451	CF295451 30DGS--05
C 31	10	47.6	30	4	BM392665	BM392665 50071-2-1
C 32	10	47.6	30	4	BM392665	BM392665 50071-2-1
C 33	9.8	46.7	22	1	AI153141	AI153141 uds5a10.r
C 34	9.8	46.7	23	8	AZ810074	AZ810074 2M0074J19
C 35	9.8	46.7	23	8	AZ810074	AZ810074 2M0074J19
C 36	9.8	46.7	23	8	AZ810074	AZ810074 2M0074J19
C 37	9.8	46.7	25	8	AZ688136	AZ688136 1M0396E09
C 38	9.8	46.7	25	8	AZ634204	AZ634204 1M0489C24
C 39	9.8	46.7	25	8	AZ807605	AZ807605 2M0070L05
C 40	9.8	46.7	25	9	AG188322	AG188322 Pan trogl
C 41	9.8	46.7	26	9	TA310H08	TA310H08 T. brucei
C 42	9.8	46.7	26	9	TA310H08	TA310H08 T. brucei
C 43	9.8	46.7	27	8	AZ489568	AZ489568 1M0322P04
C 44	9.8	46.7	28	8	AZ641309	AZ641309 1M0503G17
C 45	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 46	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 47	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 48	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 49	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 50	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 51	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 52	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 53	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 54	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 55	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 56	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 57	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 58	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 59	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 60	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 61	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 62	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 63	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 64	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 65	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 66	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 67	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 68	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 69	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 70	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 71	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 72	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 73	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 74	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 75	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 76	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 77	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 78	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 79	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 80	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 81	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 82	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 83	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 84	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 85	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 86	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 87	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 88	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 89	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 90	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 91	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 92	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 93	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 94	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 95	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 96	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 97	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 98	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 99	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08
C 100	9.8	46.7	29	8	AZ762309	AZ762309 1M0557E08

ALIGNMENTS

RESULT 1
LOCUS CL982942/c
DEFINITION GC0170 TIGEM gene trap library Mus musculus cDNA clone 9125.5, mRNA sequence.
ACCESSION CL982942
VERSION CL982942.1 GI:52420370
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Kobellis, G., Nicolson, G., Marra, E., Barbaret, M., Sardello, M., Di Giorgio, F.P., Iovino, N., Zollo, M., Balabani, A. and Correse, R.
TITLE Tagging genes with cassette-exchange sites
JOURNAL Unpublished (2004)
COMMENT Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene trap.

FEATURES

source
1. 30
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="9125.5"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="B14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

ORIGIN

Query Match 60.0%; Score 12.6; DB 9; Length 30;
Best Local Similarity 63.2%; Pred. No. 2.4e+05;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGACCCGACGAGUCUCUT 20
 Db 27 AGATTTCGACGTCCTCT 9

RESULT 2
 A2821702 28 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0094001R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0094001 R, genomic survey sequence.
 A2821702
 ACCESSION A2821702.1 GI:12991610
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0094 row: 0 column: 01
 Seq primer: CACACGGAACGCGCATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0094001"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42N, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI:473214|gb|AF12972.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 58.1%; Score 12.2; DB 8; Length 28;
 Best Local Similarity 58.8%; Pred. No. 3.8e+05;
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GACCCGACGAGUCUCUT 20
 Db 1 GACCTGCCAATCTATT 17

RESULT 3
 AG192441 28 bp DNA linear GSS 06-MAR-2004
 LOCUS pan troglodytes DNA, clone: RP43-068P22.T7, genomic survey
 DEFINITION sequence.
 AG192441
 ACCESSION AG192441.1 GI:45224617
 VERSION
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 1 (bases 1 to 28)
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of library RP-43
 Unpublished
 2 (bases 1 to 28)
 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
 (E-mail:redstone@mail.krrib.re.kr, URL:http://pns.grc.krrib.re.kr/,
 Tel:82-42-866-7181, Fax:82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..28
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-068P22.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
 Query Match 58.1%; Score 12.2; DB 9; Length 28;
 Best Local Similarity 58.8%; Pred. No. 3.8e+05;
 Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGACCCGACGAGUCUCU 19
 Db 12 GTCATGCGCATGCTCT 28

RESULT 4
 A1370776 28 bp mRNA linear EST 16-FEB-1999
 LOCUS A1370776
 DEFINITION q289c10.x1 Soares pregnant uterus NbHPV Homo sapiens cDNA clone
 IMAGE:2041746.3' similar to SW:IF6G HUMAN 004637 EUKARYOTIC
 TRANSLATION INITIATION FACTOR 4 GAMMA.; mRNA sequence.
 A1370776
 ACCESSION A1370776.1 GI:4149529
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 28)
 NCBI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNLN; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 1306 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2041746"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Soares_pregnant_uterus_NbHPU"
 /note="Organ: uterus; Vector: pT73-Pac; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 AACTGGAGATTCGCGCGCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

ORIGIN
 Query Match 55.2%; Score 11.6; DB 1; Length 28;
 Best Local Similarity 61.1%; Pred. No. 7.4e+05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 2 AGGACCGCCAGCGUCUCU 19
 20 AGGACCTACGCGCTCT 3

Db
 20 AGGACCTACGCGCTCT 3

RESULT 5
 AJ592231 22 bp DNA linear GSS 15-JAN-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence, clone
 DEFINITION 609C01, genomic survey sequence.
 ACCESSION AJ592231
 VERSION AJ592231.1 GI:37941855
 KEYWORDS GSS; right border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., Depoix, R., Pelletier, G.,
 Lepoint, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL
 MEDLINE 22363535
 PUBMED 12446565
 2 (bases 1 to 22)
 Balzerque, S.
 Direct Submision
 Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border

COMMENT

to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
<http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has
 been generated in the framework of the French plant genomics
 program 'Genoplante' (<http://www.genoplante.com> and
<http://genoplante-info.inbio.gen.fr>).
 Location/Qualifiers
 1..22
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /cultivar="Massiliaeskija"
 /db_xref="taxon:3702"
 /clone="609C01"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 1..22
 /note="T-DNA flanking sequence
 right border"

ORIGIN
 Query Match 52.4%; Score 11; DB 9; Length 22;
 Best Local Similarity 57.9%; Pred. No. 1.4e+06;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 3 GGACCGCCAGCGUCUTT 21
 3 GGGACTGCCACGCTCTT 21

Db
 3 GGACCGCCAGCGUCUTT 21
 3 GGGACTGCCACGCTCTT 21

RESULT 6
 AZ847949 29 bp DNA linear GSS 21-FEB-2001
 LOCUS 2M0148B23R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION clone UGCGM0148B23 R, genomic survey sequence.
 ACCESSION AZ847949
 VERSION AZ847949.1 GI:13029307
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 29)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islem, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
 Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0148 row: B column: 23
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 29.
 Location/Qualifiers
 1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0148B23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"

FEATURES
 source

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.4%; Score 11; DB 8; Length 29;
Best Local Similarity 57.9%; Pred. No. 1.4e+06;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGACCTGCGCAGGCGCCTT 20
| ||||| : |||
Db 8 ATGACCTGCGCATGATCAT 26

RESULT 7
A2815857/c 26 bp DNA linear GSS 20-FEB-2001
LOCUS 2M008401F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGM008401 F, genomic survey sequence.

ACCESSION A2815857
VERSION A2815857.1 GI:12985765

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

TITLE

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std. Error: 0.00
Plate: 0084 row: A column: 01
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

SOURCE

1.26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM008401"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 26;
Best Local Similarity 64.3%; Pred. No. 1.8e+06;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 8 UGCCAGGCGCTT 21
: ||||| : |||
Db 19 TGCCAGGCGGTCTTT 6

RESULT 8
A2617463/c 24 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0448F1SR Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0448F1S R, genomic survey sequence.

ACCESSION A2617463
VERSION A2617463.1 GI:11739653

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

TITLE

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std. Error: 0.00
Plate: 0448 row: F column: 15
Seq primer: CACACGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

SOURCE

1.24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0448F1S"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.5%; Score 10.6; DB 8; Length 24;
Best Local Similarity 70.6%; Pred. No. 2.2e+06;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGGACCCGCGCAGUCUC 18
|||:|||||
Db 18 AGGACTGCCACGCAC 2

RESULT 9
AL042578 28 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZP434J0821.F1.434 (synonym: htes3) Homo sapiens cDNA clone

ACCESSION AL042578
VERSION AL042578.1 GI:49682446

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 28)
Blum, H., Bauersachs, S., Mewes, H.W., Gaassenhuber, J. and Wiemann, S.

AUTHORS EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

1..28
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="DKFZP434J0821"
/issue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 49.5%; Score 10.4; DB 1; Length 28;
Best Local Similarity 61.5%; Pred. No. 2.8e+06;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCUGCCAGUCUC 18
|||:|||||
Db 3 CCGCCGCTACTC 15

RESULT 10
AZ642513

LOCUS AZ642513 28 bp DNA linear GSS 14-DEC-2000
DEFINITION IN0505N01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0505N01 R, genomic survey sequence.

ACCESSION AZ642513
VERSION AZ642513.1 GI:11769194
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0505 row: N column: 01
Seq primer: CACACGGAACAGCTATGACC
Clase: plasmid ends
High quality sequence stop: 28.

FEATURES

Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0505N01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 28;
Best Local Similarity 75.0%; Pred. No. 2.8e+06;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCCAGUCUCUT 20
|||||:|||||
Db 3 GCCAGAGCTCTT 14

RESULT 11
AZ64477/c

LOCUS AZ454477 29 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM02556N22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M02556N22 F, genomic survey sequence.
 ACCESSION AZ454477
 VERSION AZ454477.1 GI:10612602
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0256 row: N column: 22
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 29.
 FEATURES
 source
 1..29
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0256N22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|47321419b|AF12972.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

LOCUS BG424013 30 bp mRNA linear EST 14-MAR-2001
 DEFINITION 602447475F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4586106 5',
 mRNA sequence.
 ACCESSION BG424013
 VERSION BG424013.1 GI:13330519
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE NIH-MGC http://mhc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHCN1314 row: e column: 19
 High quality sequence stop: 30.
 FEATURES
 source
 1..30
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4586106"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 14"
 /note="Organ: Kidney; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGACG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
 Query Match 49.5%; Score 10.4; DB 8; Length 29;
 Best Local Similarity 75.0%; Pred. No. 2.8e+06;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

ORIGIN
 Query Match 49.5%; Score 10.4; DB 4; Length 30;
 Best Local Similarity 55.0%; Pred. No. 2.8e+06;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0422 row: L column: 13
Seq primer: CGTTGTAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers

1..22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M0422L13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid U081M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match

48.6%; Score 10.2; DB 8; Length 22;

Best Local Similarity 53.3%; Pred. No. 3.4e+06;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCUGCCAGUCGUCUT 20

Db 18 CTTTCCCTGCTCTT 4

RESULT 14
AA937308/c
LOCUS
DEFINITION

AA937308 28 bp mRNA linear EST 10-JUN-1998
IMAGE:1541243.3, similar to SW:BNCL_RAT P02683 BRAIN NEURON
CYTOPLASMIC PROTEIN 1; mRNA sequence.

ACCESSION
AA937308
VERSION
AA937308.1 GI:3095419

KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 28)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: cga@ds-f@mail.nih.gov

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert length: 987 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..28

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1541243"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CCAP GCBI) were mixed, and 88 clones were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1. M.A.G.E. clones 297460-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match

48.6%; Score 10.2; DB 1; Length 28;

Best Local Similarity 73.3%; Pred. No. 3.5e+06;

Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGGACCCGACGUC 16

Db 28 AGGACACCCGCTGC 14

RESULT 15
AB004341

LOCUS
DEFINITION
AB004341 28 bp DNA linear GSS 24-JUL-1997
Mouse genomic DNA, chromosome 17, clone YAC ymwIBR121D10, genomic
survey sequence.

ACCESSION
AB004341
VERSION
AB004341.1 GI:2242909

KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (sites)
Yoshino, M., Xiao, H., Jones, E., Trachtulec, Z., Vincel, V.,
A YAC contig from the distal Mnc class I region on mouse Chr17

TITLE
Unpublished
2 (bases 1 to 28)

JOURNAL
Yoshino, M.
Direct Submissions

TITLE
Submitted (29-MAY-1997) Masayasu Yoshino, U.T. Southwestern Medical
Center, HHMI, 5323 Harry Hines Blvd, Dallas, TX 75225-9050, USA
(E-mail: YOSHINO@UTSW.SWEMD.EDU, Tel:214-648-5047, Fax:214-648-5453)

FEATURES

source

Location/Qualifiers

1..28

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="17"
/clone="YAC ymwIBR121D10"
/haplotype="H2b"
/clone_lib="the MIT mouse YAC library; cat.#95021 Research
Genetics"
/note="right arm portion of the clone"

ORIGIN

Query Match 48.6%; Score 10.2; DB 9; Length 28;
 Best Local Similarity 53.3%; Pred. No. 3.5e+06;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 5 ACCUGCCAGUGUCU 19
 |||:|||||:|:|:
 Db 10 ACCUGCCACTTCTT 24

Search completed: September 30, 2005, 11:04:02
 Job time : 2992 secs